

In the claims:

Please amend the claims as follows:

1. (Previously Amended) A substantially pure polypeptide comprising an amino acid sequence at least 76% identical to SEQ ID NO:1, wherein the polypeptide is a transporter of an organic cation.
2. (Previously Amended) The polypeptide of claim 1, wherein the amino acid sequence is at least 80% identical to SEQ ID NO:1.
3. (Previously Amended) The polypeptide of claim 1, wherein the amino acid sequence is at least 90% identical to SEQ ID NO:1.
4. (Previously Amended) The polypeptide of claim 1, wherein the amino acid sequence is at least 95% identical to SEQ ID NO:1.
5. (Previously Amended) A substantially pure polypeptide comprising the sequence of SEQ ID NO:1.
6. (Previously Amended) A substantially pure polypeptide comprising the amino acid sequence of SEQ ID NO:1, with up to 30 conservative amino acid substitutions, wherein the polypeptide is a transporter of an organic cation.
7. (Previously Amended) A substantially pure polypeptide encoded by a nucleic acid that hybridizes to a probe the sequence of which consists of SEQ ID NO:2, under conditions of: hybridization at 68°, followed by washing in 2 x SSC/0.1% SDS for 20 minutes at room temperature and twice in 0.1 X SSC/0.1% SDS for 20 minutes at 50°, wherein the polypeptide is a transporter of an organic cation.

29. (Previously Added) A substantially pure polypeptide consisting of the sequence of SEQ ID NO:1.

30. (Currently Amended) A substantially pure polypeptide comprising an amino acid sequence at least 76% identical to SEQ ID NO:1, wherein the polypeptide is a transporter of an organic cation, and wherein the polypeptide has a ~~transporter consensus sequence~~ comprises the sequence: Xaa1-Xaa2-Xaa3-Xaa4-Xaa5-Xaa6- Xaa7-Gly-Arg-Xaa8-Xaa9-Xaa10-Xaa11-Xaa12, wherein

Xaa1 is Leu, Ile, Val, Met, Ser, Thr, Ala, or Gly;

Xaa2 is Leu, Ile, Val, Met, Phe, Ser, Ala, or Gly;

Xaa3 is any amino acid;

Xaa4 is Leu, Ile, Val, Met, Ser, Ala;

Xaa5 is Asp or Glu;

Xaa6 is any amino acid;

Xaa7 is Leu, Ile, Val, Met, Phe, Tyr, Trp, or Ala;

Xaa8 is Arg or Lys;

Xaa9 is any amino acid;

Xaa10 is any amino acid;

Xaa11 is any amino acid; and

Xaa12 is Gly, Ser, Thr, or Ala.

31. (Previously Added) A substantially pure polypeptide comprising an amino acid sequence at least 76% identical to SEQ ID NO:1, wherein the polypeptide is a transporter of an organic cation, and wherein the polypeptide has 11 to 12 transmembrane domains.

32. (Currently Amended) A substantially pure polypeptide comprising an amino acid sequence at least 76% identical to SEQ ID NO:1, wherein the polypeptide is a transporter of an organic cation, and wherein the polypeptide has a GTP/ATP binding domain ([Ala, Gly]-Xaa(4)-Gly-Lys-[Ser, Thr]).

33. (Currently Amended) A substantially pure polypeptide comprising an amino acid sequence at least 76% identical to SEQ ID NO:1, wherein the polypeptide is a transporter of an organic cation, and wherein the polypeptide has (a) 11 to 12 transmembrane domains, (b) a GTP/ATP binding domain ([Ala, Gly]-Xaa(4)-Gly-Lys-[Ser, Thr], and (c) ~~a transporter consensus~~ the sequence: Xaa1-Xaa2-Xaa3-Xaa4-Xaa5-Xaa6- Xaa7-Gly-Arg-Xaa8-Xaa9-Xaa10-Xaa11-Xaa12, wherein

Xaa is any amino acid;

Xaa1 is Leu, Ile, Val, Met, Ser, Thr, Ala, or Gly;

Xaa2 is Leu, Ile, Val, Met, Phe, Ser, Ala, or Gly;

Xaa3 is any amino acid;

Xaa4 is Leu, Ile, Val, Met, Ser, Ala;

Xaa5 is Asp or Glu;

Xaa6 is any amino acid;

Xaa7 is Leu, Ile, Val, Met, Phe, Tyr, Trp, or Ala;

Xaa8 is Arg or Lys;

Xaa9 is any amino acid;

Xaa10 is any amino acid;

Xaa11 is any amino acid; and

Xaa12 is Gly, Ser, Thr, or Ala.

34. (Previously Added) A substantially pure human transport polypeptide comprising an amino acid sequence at least 76% identical to SEQ ID NO:1, wherein the polypeptide is a transporter of an organic cation, and wherein the polypeptide has (a) 11 to 12 transmembrane domains, (b) a GTP/ATP binding domain ([Ala, Gly]-Xaa(4)-Gly-Lys-[Ser, Thr], and (c) ~~a transporter consensus~~ the sequence: Xaa1-Xaa2-Xaa3-Xaa4-Xaa5-Xaa6- Xaa7-Gly-Arg-Xaa8-Xaa9-Xaa10-Xaa11-Xaa12, wherein

Xaa is any amino acid;

Xaa1 is Leu, Ile, Val, Met, Ser, Thr, Ala, or Gly;

Xaa2 is Leu, Ile, Val, Met, Phe, Ser, Ala, or Gly;

Xaa3 is any amino acid;

Xaa4 is Leu, Ile, Val, Met, Ser, or Ala;

Xaa5 is Asp or Glu;

Xaa6 is any amino acid;

Xaa7 is Leu, Ile, Val, Met, Phe, Tyr, Trp, or Ala;

Xaa8 is Arg or Lys;

Xaa9 is any amino acid;

Xaa10 is any amino acid;

Xaa11 is any amino acid; and

Xaa12 is Gly, Ser, Thr, or Ala.

35. (New) The polypeptide of claim 30, wherein the amino acid sequence at least 80% identical to SEQ ID NO:1.

36. (New) The polypeptide of claim 30, wherein the amino acid sequence at least 90% identical to SEQ ID NO:1.

37 (New) The polypeptide of claim 30, wherein the amino acid sequence at least 95% identical to SEQ ID NO:1.

38. (New) The polypeptide of claim 31, wherein the amino acid sequence at least 80% identical to SEQ ID NO:1.

39. (New) The polypeptide of claim 31, wherein the amino acid sequence at least 90% identical to SEQ ID NO:1.

40. (New) The polypeptide of claim 31, wherein the amino acid sequence at least 95% identical to SEQ ID NO:1.

41. (New) The polypeptide of claim 32, wherein the amino acid sequence at least 80% identical to SEQ ID NO:1.

42. (New) The polypeptide of claim 32, wherein the amino acid sequence at least 90% identical to SEQ ID NO:1.

43. (New) The polypeptide of claim 32, wherein the amino acid sequence at least 95% identical to SEQ ID NO:1.

44. (New) The polypeptide of claim 33, wherein the amino acid sequence at least 80% identical to SEQ ID NO:1.

45. (New) The polypeptide of claim 33, wherein the amino acid sequence at least 90% identical to SEQ ID NO:1.

46. (New) The polypeptide of claim 33, wherein the amino acid sequence at least 95% identical to SEQ ID NO:1.

47. (New) The polypeptide of claim 34, wherein the amino acid sequence at least 80% identical to SEQ ID NO:1.

48. (New) The polypeptide of claim 34, wherein the amino acid sequence at least 90% identical to SEQ ID NO:1.

49. (New) The polypeptide of claim 34, wherein the amino acid sequence at least 95% identical to SEQ ID NO:1.